SPECIFICATION AMENDMENTS

Please replace page 28, line 1 through page 29, line 21 to read as follows:

Five different mutations of the 3-phosphoglycerate-dehydrogenase of *C. glutamicum* were produced which had deletions of different lengths at the C terminal (FIG. 2). The construction of the deletion mutant is carried out in the same manner as the isolation of the wild type *serA*- gene by means of PCR. For this purpose, a PCR primer (*serA*-f: 5'-TCTAGAGCCGGAGACGTGAATAAAAT-3'){SEQ ID NO: 13} is produced, the homologue being to a region 240 bp prior to the start codon of the gene to encompass the entire promoter region. This primer is used for all constructs and carries at the 3' end a cutting site for the restriction enzyme XbaI. For the amplification of the complete *serA* gene, a second reverse complementary primer is selected which lies 199 bp behind the stop codon and carries a *Bam*HI restriction site (*serA*-r: 5' GGATCCGACTGGTGAGGGTCAAGTCC-3') [SEQ ID NO: 14].

The expected PCR product has a length of 2040 bp. To produce the deletion, a reverse complementary primer is selected which lies in the gene region and carries a restriction site for *BAMH*I. The primer *serA*Δ211-r (5'-GGATCCTTAACCGGAAACGTTCACAGC-3'){SEQ ID NO: 15] lies 956 bp behind the start codon so that a PCR product with a length of 1196 bp results. The last 211 amino acids

of the 3-phosphoglycerate-dehydrogenase are cut off. The deletion lies generally in the region of the assumed transition from the substrate binding domain to the regulatory domain (compare FIGS. 1 and 2). The primer *serA*Δ205-r (5'-GGATCCTTACTCTTCGCCCACGCGACC-3')[SEQ ID NO: 16] lies 974 bp behind the start codon and the expected PCR product has a length of 1214 bp. The C terminal deletion in this case amounts to 204 amino acids and the protein terminates behind the amino acid glutamate at position 325. The undirected exchange of this amino acid to lysine produces in *C. glutamicum* a deregulation of the 3-phosphoglycerate-dehydrogenase (EP 0 931 833). Both deletions lie in a region in which the deletion (Δ209 amino acids) of rat protein has been produced. Achouri Y., Rider M.H., Van Schaftingen E. and Robbi M., 1997, Biochem J., 323-365-370. Both primers *serA*Δ197-r (5'-GGATACCTTAAGCCAGAATCCATCCACACAG-3')[SEQ ID NO: 17] and *serA*Δ188-r (5'-GGATCCTTACTTGCCAGCAAGAAAAGACC-3') [SEQ ID NO: 18] lie 998 bp or 1025 bp behind the ATG and find themselves upstream from the transition from the substrate binding domain to the regulatory domain in *E. coli*. The polypeptide chain produced from the DNA fragment expected from the PCR is shorter by 197 or 188 corresponding amino acids than the full 3-phosphoglycerate-dehydrogenase. The shortest deletion is produced by the primer *serA*Δ79-r (5'-GGATCCTTAATCCAGGCCACGGCCATT-3')[SEQ ID NO: 19] and cuts out the region of 79 amino acids which has the greatest similarity to the regulatory domain of *E. coli*. In addition in all

of the reverse complementary primers, which give rise to a shortened protein, behind the restriction site, the stop code TAA is introduced.

The preceding seven primers have been assigned the respective designations: SEQ ID No. 13, SEQ ID No. 14, SEQ ID No. 15, SEQ ID No. 16, SEQ ID No. 17, SEQ ID No. 18 and SEQ ID No. 19.